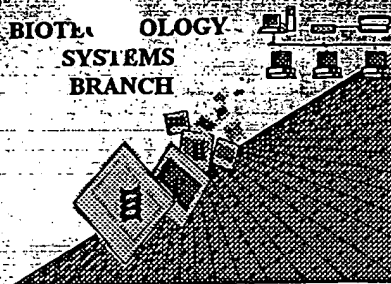


R Zeman #1 SK 8/17/00

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/461,580

Source: 1645

Date Processed by STIC: 7-26-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/46/580

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

MAY 16 2000

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

R. Zeman

Does Not Comply
Corrected Diskette Needed

1645

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AUG 16 2000

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/461,580
DATE: 07/26/2000
TIME: 14:00:15

Input Set : A:\00501618000.txt
Output Set: N:\CRF3\07262000\I461580.raw

4 <110> APPLICANT: Guarente, Leonard
5 Imai, Shin-ichiro
6 Armstrong, Christopher
8 <120> TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
9 ALTER HISTINE PROTEIN ACETYLATION, DECREASE AGING, INCREASE
10 LIFESPAN
12 <130> FILE REFERENCE: 0050.1618-000
14 <140> CURRENT APPLICATION NUMBER: 09/461,580
15 <141> CURRENT FILING DATE: 1999-12-15
17 <160> NUMBER OF SEQ ID NOS: 35
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 737
23 <212> TYPE: PRT
24 <213> ORGANISM: Mus musculus
26 <400> SEQUENCE: 1
27 Met Ala Asp Glu Val Ala Leu Ala Leu Gln Ala Ala Gly Ser Pro Ser
28 1 5 10 15
29 Ala Ala Ala Ala Met Glu Ala Ala Ser Gln Pro Ala Asp Glu Pro Leu
30 20 25 30
31 Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Gly Arg Ser Pro Gly
32 35 40 45
33 Glu Pro Ser Ala Ala Val Ala Pro Ala Ala Ala Gly Cys Glu Ala Ala
34 50 55 60
35 Ser Ala Ala Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala
36 65 70 75 80
37 Ala Ser Ala Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly
38 85 90 95
39 Asp Asn Gly Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe
40 100 105 110
41 Asp Asp Asp Glu Gly Glu Glu Glu Asp Glu Ala Ala Ala Ala Ala Ala
42 115 120 125
43 Ala Ala Ala Ile Gly Tyr Arg Asp Asn Leu Leu Thr Asp Gly Leu
44 130 135 140
45 Leu Thr Asn Gly Phe His Ser Cys Glu Ser Asp Asp Asp Arg Thr
46 145 150 155 160
47 Ser His Ala Ser Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro
48 165 170 175
49 Tyr Thr Phe Val Gln Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr
50 180 185 190
51 Ile Leu Lys Asp Leu Leu Pro Glu Thr Ile Pro Pro Glu Leu Asp
52 195 200 205
53 Asp Met Thr Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro
54 210 215 220
55 Lys Arg Lys Lys Arg Lys Asp Ile Asn Thr Ile Glu Asp Ala Val Lys
56 225 230 235 240
57 Leu Leu Gln Glu Cys Lys Lys Ile Ile Val Leu Thr Gly Ala Gly Val

See p. 5, 7

RAW SEQUENCE LISTING

DATE: 07/26/2000

PATENT APPLICATION: US/09/461,580

TIME: 14:00:15

Input Set : A:\00501618000.txt

Output Set: N:\CRF3\07262000\I461580.raw

```

58                               245                               250                               255
59 Ser Val Ser Cys Gly Ile Pro Asp Phe Arg Ser Arg Asp Gly Ile Tyr
60                               260                               265                               270
61 Ala Arg Leu Ala Val Asp Phe Pro Asp Leu Pro Asp Pro Gln Ala Met
62                               275                               280                               285
63 Phe Asp Ile Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys Phe
64                               290                               295                               300
65 Ala Lys Glu Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His Lys
66 305                               310                               315                               320
67 Phe Ile Ala Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr Thr
68                               325                               330                               335
69 Gln Asn Ile Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile Leu
70                               340                               345                               350
71 Gln Cys His Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys Tyr
72                               355                               360                               365
73 Lys Val Asp Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val Val
74                               370                               375                               380
75 Pro Arg Cys Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met Lys
76 385                               390                               395                               400
77 Pro Glu Ile Val Phe Phe Gly Glu Asn Leu Pro Glu Gln Phe His Arg
78                               405                               410                               415
79 Ala Met Lys Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile Gly
80                               420                               425                               430
81 Ser Ser Leu Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile Pro
82                               435                               440                               445
83 His Glu Val Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His Leu
84                               450                               455                               460
85 His Phe Asp Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn Glu
86 465                               470                               475                               480
87 Leu Cys His Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn Pro
88                               485                               490                               495
89 Val Lys Leu Ser Glu Ile Thr Glu Lys Pro Pro Arg Pro Gln Lys Glu
90                               500                               505                               510
91 Leu Val His Leu Ser Glu Leu Pro Thr Pro Leu His Ile Ser Glu
92                               515                               520                               525
93 Asp Ser Ser Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile
94                               530                               535                               540
95 Ala Thr Leu Val Asp Gln Ala Thr Asn Asn Asn Val Asn Asp Leu Glu
96 545                               550                               555                               560
97 Val Ser Glu Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr
98                               565                               570                               575
99 Ser Arg Asn Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala
100                               580                               585                               590
101 Val Gly Ser Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu
102                               595                               600                               605
103 Thr Val Arg Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser
104                               610                               615                               620
105 Lys Arg Leu Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr
106 625                               630                               635                               640

```

RAW SEQUENCE LISTING DATE: 07/26/2000
 PATENT APPLICATION: US/09/461,580 TIME: 14:00:15

Input Set : A:\00501618000.txt
 Output Set: N:\CRF3\07262000\I461580.raw

```

107 Ile Phe His Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu
108                               645 650 655
110 Ser Ser Ser Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser
111                               660 665 670
112 Pro Ser Leu Glu Glu Pro Leu Glu Asp Glu Ser Glu Ile Glu Glu Phe
113                               675 680 685
114 Tyr Asn Gly Leu Glu Asp Asp Thr Glu Arg Pro Glu Cys Ala Gly Gly
115                               690 695 700
116 Ser Gly Phe Gly Ala Asp Gly Gly Asp Gln Glu Val Val Asn Glu Ala
117 705                               710 715 720
118 Ile Ala Thr Arg Gln Glu Leu Thr Asp Val Asn Tyr Pro Ser Asp Lys
119                               725 730 735
120 Ser
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 272
126 <212> TYPE: PRT
127 <213> ORGANISM: Saccharomyces cerevisiae
129 <400> SEQUENCE: 2
130 Ile Asn Lys Val Leu Cys Thr Arg Leu Arg Leu Ser Asn Phe Phe Thr
131 1 5 10 15
132 Ile Asp His Phe Ile Gln Lys Leu His Thr Ala Arg Lys Ile Leu Val
133 20 25 30
134 Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg
135 35 40 45
136 Ser Ser Glu Gly Phe Tyr Ser Lys Ile Lys His Leu Gly Leu Asp Asp
137 50 55 60
138 Pro Gln Asp Val Phe Asn Tyr Asn Ile Phe Met His Asp Pro Ser Val
139 65 70 75 80
140 Phe Tyr Asn Ile Ala Asn Met Val Leu Pro Pro Glu Lys Ile Tyr Ser
141 85 90 95
142 Pro Leu His Ser Phe Ile Lys Met Leu Gln Met Lys Gly Lys Leu Leu
143 100 105 110
144 Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile
145 115 120 125
146 Ser Thr Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Thr
147 130 135 140
148 Cys Val Thr Cys His Trp Asn Leu Pro Gly Glu Arg Ile Phe Asn Lys
149 145 150 155 160
150 Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Lys Lys Arg
151 165 170 175
152 Arg Glu Tyr Phe Pro Glu Gly Tyr Asn Asn Lys Val Gly Val Ala Ala
153 180 185 190
154 Ser Gln Gly Ser Met Ser Glu Arg Pro Pro Tyr Ile Leu Asn Ser Tyr
155 195 200 205
156 Gly Val Leu Lys Pro Asp Ile Thr Phe Phe Gly Glu Ala Leu Pro Asn
157 210 215 220
158 Lys Phe His Lys Ser Ile Arg Glu Asp Ile Leu Glu Cys Asp Leu Leu
159 225 230 235 240
160 Ile Cys Ile Gly Thr Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val

```

RECEIVED
 AUG 16 2000
 TECH CENTER 16002000

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/461,580
 DATE: 07/26/2000
 TIME: 14:00:15

Input Set : A:\00501618000.txt
 Output Set: N:\CRF3\07262000\I461580.raw

```

161                               245                               250                               255
162 Asn Met Val Pro Ser His Val Pro Gln Val Leu Ile Asn Arg Asp Pro
163                               260                               265                               270
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 267
168 <212> TYPE: PRT /
169 <213> ORGANISM: Saccharomyces cerevisiae /
171 <400> SEQUENCE: 3
172 Ile Asn Lys Val Leu Ser Thr Arg Leu Arg Leu Pro Asn Phe Asn Thr
173 1 5 10 15
174 Ile Asp His Phe Thr Ala Thr Leu Arg Asn Ala Lys Lys Ile Leu Val
175 20 25 30
176 Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg
177 35 40 45
178 Ser Ser Glu Gly Phe Tyr Ser Lys Ile Arg His Leu Gly Leu Glu Asp
179 50 55 60
180 Pro Gln Asp Val Phe Asn Leu Asp Ile Phe Leu Gln Asp Pro Ser Val
181 65 70 75 80
182 Phe Tyr Asn Ile Ala His Met Val Leu Pro Pro Glu Asn Met Tyr Ser
183 85 90 95
184 Pro Leu His Ser Phe Ile Lys Met Leu Gln Asp Lys Gly Lys Leu Leu
185 100 105 110
186 Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile
187 115 120 125
188 Asp Pro Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Ser
189 130 135 140
190 Cys Val Thr Cys His Trp Gln Ile Pro Gly Glu Lys Ile Phe Glu Asn
191 145 150 155 160
192 Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Gln Lys Arg
193 165 170 175
194 Lys Gln Tyr Phe Pro Met Ser Asn Gly Asn Asn Thr Val Gln Thr Asn
195 180 185 190
196 Ile Asn Phe Asn Ser Pro Ile Leu Lys Ser Tyr Gly Val Leu Lys Pro
197 195 200 205
198 Asp Met Thr Phe Phe Gly Glu Ala Leu Pro Ser Arg Phe His Lys Thr
199 210 215 220
200 Ile Arg Lys Asp Ile Leu Glu Cys Asp Leu Leu Ile Cys Ile Gly Thr
201 225 230 235 240
202 Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val Asn Met Val Pro Ser
203 245 250 255
204 His Val Pro Gln Ile Leu Ile Asn Arg Asp Met
205 260 265
208 <210> SEQ ID NO: 4
209 <211> LENGTH: 245
210 <212> TYPE: PRT
211 <213> ORGANISM: Mus musculus /
213 <400> SEQUENCE: 4
214 Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp
215 1 5 10 15

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/461,580

DATE: 07/26/2000

TIME: 14:00:15

Input Set : A:\00501618000.txt

Output Set: N:\CRF3\07262000\I461580.raw

```

216 Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys
217                               20                25                30
218 Ile Ile Val Leu, Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro
219                               35                40                45
221 Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe
222                               50                55                60
223 Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg
224 65                               70                75                80
225 Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly
226                               85                90                95
227 Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys
228                               100               105               110
229 Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu
230                               115               120               125
231 Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His Gly Ser Phe Ala
232                               130               135               140
233 Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val
234 145                               150               155               160
235 Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro
236                               165               170               175
237 Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Gly
238                               180               185               190
239 Glu Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp
240                               195               200               205
241 Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro
242                               210               215               220
243 Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu
244 225                               230               235               240
245 Ile Asn Arg Glu Pro
246                               245
249 <210> SEQ ID NO: 5
250 <211> LENGTH: 237
251 <212> TYPE: PRT
252 <213> ORGANISM: Escherichia coli
254 <400> SEQUENCE: 5
255 Met Met Glu Asn Pro Arg Val Leu Val Leu Thr Gly Ala Gly Ile Ser
256 1                               5                10                15
257 Ala Glu Ser Gly Ile Arg Thr Phe Arg Ala Ala Asp Gly Leu Trp Glu
258                               20                25                30
259 Glu His Arg Val Glu Asp Val Ala Thr Pro Glu Gly Phe Ala Arg Asn
260                               35                40                45
261 Pro Gly Leu Val Gln Thr Phe Tyr Asn Ala Arg Arg Gln Gln Leu Gln
262 50                               55                60
263 Gln Pro Glu Ile Gln Pro Asn Ala Ala His Leu Ala Leu Ala Asn Leu
264 65                               70                75                80
265 Lys Lys Arg Leu Ala Ile Ala Phe Leu Leu Val Thr Gln Asn Ile Asp
266                               85                90                95
267 Asn Leu His Glu Arg Ala Gly Asn Arg Asn Ile Ile Gln Met His Gly
268                               100               105               110

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

<210> 35
 <211> 232
 <212> PRT
 <213> unknown

*Mandatory feature missing.
 You must have <220> <223>
 features to explain origin of Unknown*

organism

See #12

on Error

*Summary
 Sheet*

<400> 35
 Thr Arg Pro Arg Thr Arg Gly His Gly Thr Glu Gln Ser Val Thr Val
 1 5 10 15
 Pro Arg Ala Pro Thr Pro Phe Pro Trp Pro Ser Arg Thr Asp Ser Asp
 20 25 30
 Ser Asp Thr Glu Gly Gly Ala Thr Gly Gly Glu Ala Glu Met Asp Phe
 35 40 45
 Leu Arg Asn Leu Phe Thr Gln Thr Leu Gly Leu Gly Ser Gln Lys Glu
 50 55 60
 Arg Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Thr Arg Tyr Met Gln
 65 70 75 80
 Ser Glu Arg Cys Arg Lys Val Ile Cys Leu Val Gly Ala Gly Ile Ser
 85 90 95
 Thr Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr
 100 105 110
 Ala Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu
 115 120 125
 Ile Ser Tyr Phe Lys Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys
 130 135 140
 Glu Leu Tyr Pro Gly Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Ile
 145 150 155 160
 Arg Leu Leu Lys Glu Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn
 165 170 175
 Ile Asp Thr Leu Glu Arg Val Ala Gly Leu Glu Pro Gln Asp Leu Val
 180 185 190
 Glu Ala His Gly Thr Phe Tyr Thr Ser His Cys Val Asn Thr Ser Cys
 195 200 205
 Arg Lys Glu Tyr Thr Met Gly Trp Met Lys Glu Lys Ile Ser Gln Lys
 210 215 220
 Gln Leu Pro Gly Val Ser Ser Val
 225 230

VERIFICATION SUMMARY DATE: 07/26/2000
PATENT APPLICATION: US/09/461,580 TIME: 14:00:16

Input Set : A:\00501618000.txt
Output Set: N:\CRF3\07262000\I461580.raw

L:1110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1261 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 34
L:1270 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1270 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: .